saturation mutagenesis of said genome by insertion mutagenesis, whereby an oligonucleotide sequence tag is inserted into said target region such that a population of DNA molecules is obtained having at least 90% of nucleotide positions of said target region insertionally mutated;

introducing said population of mutagenized DNA molecules into host cells that express said sequence of interest;

subjecting a first aliquot of said host cells to at least one selective condition and a second aliquot to a non-selective condition thereby providing at least one selected and one non-selected aliquot;

amplifying said target region from said at least one selected and one non-selected aliquots, using a first primer hybridizing to said sequence tag and a second primer hybridizing to a known endpoint, said endpoint being characterized as an arbitrary unique sequence in said target DNA, thereby giving rise to amplified DNA; and

resolving by gel electrophoresis said amplified DNA from said at least one selected and one non-selected aliquots into individual bands which differ by size, to identify the position of individual sequence tag insertions within said target region,

whereby differences between the presence or intensity of bands between said at least one selected and one non-selected aliquots are indicative that said sequence tag insertion causes a difference in response to said selective condition thereby functionally identifying said target region under said at least one selected condition .

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12. (AMENDED) A method according to claim 4 , whereby the absence of a band under said selective condition and its presence under non-selective conditions is indicative of a target region which is essential under said selective condition.

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21. (NEW) A method according to claim 4, wherein said haploid genome is a bacterial genome.
